

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5 (i) APPLICANT: Ashkenazi, Avi J.  
Baker, Kevin  
Gurney, Austin  
Wood, William

10 (ii) TITLE OF INVENTION: Apo-2DcR

(iii) NUMBER OF SEQUENCES: 13

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genentech, Inc.  
(B) STREET: 460 Point San Bruno Blvd  
(C) CITY: South San Francisco  
(D) STATE: California  
(E) COUNTRY: USA  
(F) ZIP: 94080

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: WinPatin (Genentech)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
30 (B) FILING DATE: 18-Jun-1997  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Marschang, Diane L.  
35 (B) REGISTRATION NUMBER: 35,600

(C) REFERENCE/DOCKET NUMBER: P1110

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 415/225-5416

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(C) TELEX: 910/371-7168

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 259 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Ala	Arg	Ile	Pro	Lys	Thr	Leu	Lys	Phe	Val	Val	Val	Ile	Val
1				5					10					15
Ala	Val	Leu	Leu	Pro	Val	Leu	Ala	Tyr	Ser	Ala	Thr	Thr	Ala	Arg
				20					25					30
Gln	Glu	Glu	Val	Pro	Gln	Gln	Thr	Val	Ala	Pro	Gln	Gln	Gln	Arg
				35					40					45
His	Ser	Phe	Lys	Gly	Glu	Glu	Cys	Pro	Ala	Gly	Ser	His	Arg	Ser
				50					55					60
Glu	His	Thr	Gly	Ala	Cys	Asn	Pro	Cys	Thr	Glu	Gly	Val	Asp	Tyr
				65					70					75
Thr	Asn	Ala	Ser	Asn	Asn	Glu	Pro	Ser	Cys	Phe	Pro	Cys	Thr	Val
				80					85					90
Cys	Lys	Ser	Asp	Gln	Lys	His	Lys	Ser	Ser	Cys	Thr	Met	Thr	Arg

				95						100					105
	Asp	Thr	Val	Cys	Gln	Cys	Lys	Glu	Gly	Thr	Phe	Arg	Asn	Glu	Asn
					110					115					120
5	Ser	Pro	Glu	Met	Cys	Arg	Lys	Cys	Ser	Arg	Cys	Pro	Ser	Gly	Glu
					125					130					135
	Val	Gln	Val	Ser	Asn	Cys	Thr	Ser	Trp	Asp	Asp	Ile	Gln	Cys	Val
10					140					145					150
	Glu	Glu	Phe	Gly	Ala	Asn	Ala	Thr	Val	Glu	Thr	Pro	Ala	Ala	Glu
					155					160					165
5	Glu	Thr	Met	Asn	Thr	Ser	Pro	Gly	Thr	Pro	Ala	Pro	Ala	Ala	Glu
					170					175					180
	Glu	Thr	Met	Asn	Thr	Ser	Pro	Gly	Thr	Pro	Ala	Pro	Ala	Ala	Glu
20					185					190					195
	Glu	Thr	Met	Thr	Thr	Ser	Pro	Gly	Thr	Pro	Ala	Pro	Ala	Ala	Glu
					200					205					210
	Glu	Thr	Met	Thr	Thr	Ser	Pro	Gly	Thr	Pro	Ala	Pro	Ala	Ala	Glu
25					215					220					225
	Glu	Thr	Met	Thr	Thr	Ser	Pro	Gly	Thr	Pro	Ala	Ser	Ser	His	Tyr
					230					235					240
30	Leu	Ser	Cys	Thr	Ile	Val	Gly	Ile	Ile	Val	Leu	Ile	Val	Leu	Leu
					245					250					255
	Ile	Val	Phe	Val											
					259										

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1180 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GCTGTGGGAA CCTCTCCACG CGCACGAACT CAGCCAACGA TTTCTGATAG 50  
ATTTTTGGGA GTTTGACCAG AGATGCAAGG GGTGAAGGAG CGCTTCCTAC 100  
CGTTAGGGAA CTCTGGGGAC AGAGCGCCCC GGCCGCCTGA TGGCCGAGGC 150  
AGGGTGCGAC CCAGGACCCA GGACGGCGTC GGGAACCATA CC ATG 195  
Met  
1  
GCC CGG ATC CCC AAG ACC CTA AAG TTC GTC GTC GTC ATC 234  
Ala Arg Ile Pro Lys Thr Leu Lys Phe Val Val Val Ile  
5 10  
GTC GCG GTC CTG CTG CCA GTC CTA GCT TAC TCT GCC ACC 273  
Val Ala Val Leu Leu Pro Val Leu Ala Tyr Ser Ala Thr  
15 20 25  
ACT GCC CGG CAG GAG GAA GTT CCC CAG CAG ACA GTG GCC 312  
Thr Ala Arg Gln Glu Glu Val Pro Gln Gln Thr Val Ala  
30 35 40  
CCA CAG CAA CAG AGG CAC AGC TTC AAG GGG GAG GAG TGT 351  
Pro Gln Gln Gln Arg His Ser Phe Lys Gly Glu Glu Cys  
35

45

50

CCA GCA GGA TCT CAT AGA TCA GAA CAT ACT GGA GCC TGT 390  
Pro Ala Gly Ser His Arg Ser Glu His Thr Gly Ala Cys

5

55

60

65

AAC CCG TGC ACA GAG GGT GTG GAT TAC ACC AAC GCT TCC 429  
Asn Pro Cys Thr Glu Gly Val Asp Tyr Thr Asn Ala Ser

70

75

10

AAC AAT GAA CCT TCT TGC TTC CCA TGT ACA GTT TGT AAA 468  
Asn Asn Glu Pro Ser Cys Phe Pro Cys Thr Val Cys Lys

80

85

90

TCA GAT CAA AAA CAT AAA AGT TCC TGC ACC ATG ACC AGA 507  
Ser Asp Gln Lys His Lys Ser Ser Cys Thr Met Thr Arg

95

100

105

GAC ACA GTG TGT CAG TGT AAA GAA GGC ACC TTC CGG AAT 546  
Asp Thr Val Cys Gln Cys Lys Glu Gly Thr Phe Arg Asn

110

115

GAA AAC TCC CCA GAG ATG TGC CGG AAG TGT AGC AGG TGC 585  
Glu Asn Ser Pro Glu Met Cys Arg Lys Cys Ser Arg Cys

120

125

130

CCT AGT GGG GAA GTC CAA GTC AGT AAT TGT ACG TCC TGG 624  
Pro Ser Gly Glu Val Gln Val Ser Asn Cys Thr Ser Trp

135

140

30

GAT GAT ATC CAG TGT GTT GAA GAA TTT GGT GCC AAT GCC 663  
Asp Asp Ile Gln Cys Val Glu Glu Phe Gly Ala Asn Ala

145

150

155

35

ACT GTG GAA ACC CCA GCT GCT GAA GAG ACA ATG AAC ACC 702

Thr Val Glu Thr Pro Ala Ala Glu Glu Thr Met Asn Thr  
 160 165 170

AGC CCG GGG ACT CCT GCC CCA GCT GCT GAA GAG ACA ATG 741  
 5 Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met  
 175 180

AAC ACC AGC CCA GGG ACT CCT GCC CCA GCT GCT GAA GAG 780  
 10 Asn Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu  
 185 190 195

ACA ATG ACC ACC AGC CCG GGG ACT CCT GCC CCA GCT GCT 819  
 Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala  
 200 205

GAA GAG ACA ATG ACC ACC AGC CCG GGG ACT CCT GCC CCA 858  
 Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro  
 210 215 220

GCT GCT GAA GAG ACA ATG ACC ACC AGC CCG GGG ACT CCT 897  
 Ala Ala Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro  
 225 230 235

GCC TCT TCT CAT TAC CTC TCA TGC ACC ATC GTA GGG ATC 936  
 25 Ala Ser Ser His Tyr Leu Ser Cys Thr Ile Val Gly Ile  
 240 245

ATA GTT CTA ATT GTG CTT CTG ATT GTG TTT GTT T 970  
 Ile Val Leu Ile Val Leu Leu Ile Val Phe Val  
 30 250 255 259

GAAAGACTTC ACTGTGGAAG AAATTCCTTC CTTACCTGAA AGGTTTCAGGT 1020

AGGCGCTGGC TGAGGGCGGG GGGCGCTGGA CACTCTCTGC CCTGCCTCCC 1070

TCTGCTGTGT TCCCACAGAC AGAAACGCCT GCCCCTGCCC CAAAAAAAAA 1120  
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1170  
 5 AAAAAAAAAA 1180

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 299 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

5  
 10 Met Gln Gly Val Lys Glu Arg Phe Leu Pro Leu Gly Asn Ser Gly  
 -40 -35 -30  
 15 Asp Arg Ala Pro Arg Pro Pro Asp Gly Arg Gly Arg Val Arg Pro  
 -25 -20 -15  
 20 Arg Thr Gln Asp Gly Val Gly Asn His Thr Met Ala Arg Ile Pro  
 -10 -5 1 5  
 25 Lys Thr Leu Lys Phe Val Val Val Ile Val Ala Val Leu Leu Pro  
 10 15 20  
 30 Val Leu Ala Tyr Ser Ala Thr Thr Ala Arg Gln Glu Glu Val Pro  
 25 30 35  
 35 Gln Gln Thr Val Ala Pro Gln Gln Gln Arg His Ser Phe Lys Gly  
 40 45 50  
 40 Glu Glu Cys Pro Ala Gly Ser His Arg Ser Glu His Thr Gly Ala  
 55 60 65

	Cys	Asn	Pro	Cys	Thr	Glu	Gly	Val	Asp	Tyr	Thr	Asn	Ala	Ser	Asn
					70					75					80
5	Asn	Glu	Pro	Ser	Cys	Phe	Pro	Cys	Thr	Val	Cys	Lys	Ser	Asp	Gln
					85					90					95
	Lys	His	Lys	Ser	Ser	Cys	Thr	Met	Thr	Arg	Asp	Thr	Val	Cys	Gln
					100					105					110
10	Cys	Lys	Glu	Gly	Thr	Phe	Arg	Asn	Glu	Asn	Ser	Pro	Glu	Met	Cys
					115					120					125
	Arg	Lys	Cys	Ser	Arg	Cys	Pro	Ser	Gly	Glu	Val	Gln	Val	Ser	Asn
					130					135					140
	Cys	Thr	Ser	Trp	Asp	Asp	Ile	Gln	Cys	Val	Glu	Glu	Phe	Gly	Ala
					145					150					155
	Asn	Ala	Thr	Val	Glu	Thr	Pro	Ala	Ala	Glu	Glu	Thr	Met	Asn	Thr
20					160					165					170
	Ser	Pro	Gly	Thr	Pro	Ala	Pro	Ala	Ala	Glu	Glu	Thr	Met	Asn	Thr
					175					180					185
25	Ser	Pro	Gly	Thr	Pro	Ala	Pro	Ala	Ala	Glu	Glu	Thr	Met	Thr	Thr
					190					195					200
	Ser	Pro	Gly	Thr	Pro	Ala	Pro	Ala	Ala	Glu	Glu	Thr	Met	Thr	Thr
					205					210					215
30	Ser	Pro	Gly	Thr	Pro	Ala	Pro	Ala	Ala	Glu	Glu	Thr	Met	Thr	Thr
					220					225					230
	Ser	Pro	Gly	Thr	Pro	Ala	Ser	Ser	His	Tyr	Leu	Ser	Cys	Thr	Ile
35					235					240					245



Val Gly Ile Ile Val Leu Ile Val Leu Leu Ile Val Phe Val  
250 255 259

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1180 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCTGTGGGAA CCTCTCCACG CGCACGAACT CAGCCAACGA TTTCTGATAG 50

ATTTTTGGGA GTTTGACCAG AG ATG CAA GGG GTG AAG GAG 90  
Met Gln Gly Val Lys Glu  
-40 -35

CGC TTC CTA CCG TTA GGG AAC TCT GGG GAC AGA GCG CCC 129  
Arg Phe Leu Pro Leu Gly Asn Ser Gly Asp Arg Ala Pro  
-30 -25

CGG CCG CCT GAT GGC CGA GGC AGG GTG CGA CCC AGG ACC 168  
Arg Pro Pro Asp Gly Arg Gly Arg Val Arg Pro Arg Thr  
-20 -15 -10

CAG GAC GGC GTC GGG AAC CAT ACC ATG GCC CGG ATC CCC 207  
Gln Asp Gly Val Gly Asn His Thr Met Ala Arg Ile Pro  
-5 1 5

AAG ACC CTA AAG TTC GTC GTC GTC ATC GTC GCG GTC CTG 246  
Lys Thr Leu Lys Phe Val Val Val Ile Val Ala Val Leu  
10 15

	CTG CCA GTC CTA GCT TAC TCT GCC ACC ACT GCC CGG CAG	285
	Leu Pro Val Leu Ala Tyr Ser Ala Thr Thr Ala Arg Gln	
	20 25 30	
5	GAG GAA GTT CCC CAG CAG ACA GTG GCC CCA CAG CAA CAG	324
	Glu Glu Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln	
	35 40	
10	AGG CAC AGC TTC AAG GGG GAG GAG TGT CCA GCA GGA TCT	363
	Arg His Ser Phe Lys Gly Glu Glu Cys Pro Ala Gly Ser	
	45 50 55	
15	CAT AGA TCA GAA CAT ACT GGA GCC TGT AAC CCG TGC ACA	402
	His Arg Ser Glu His Thr Gly Ala Cys Asn Pro Cys Thr	
	60 65 70	
20	GAG GGT GTG GAT TAC ACC AAC GCT TCC AAC AAT GAA CCT	441
	Glu Gly Val Asp Tyr Thr Asn Ala Ser Asn Asn Glu Pro	
	75 80	
25	TCT TGC TTC CCA TGT ACA GTT TGT AAA TCA GAT CAA AAA	480
	Ser Cys Phe Pro Cys Thr Val Cys Lys Ser Asp Gln Lys	
	85 90 95	
30	CAT AAA AGT TCC TGC ACC ATG ACC AGA GAC ACA GTG TGT	519
	His Lys Ser Ser Cys Thr Met Thr Arg Asp Thr Val Cys	
	100 105	
35	CAG TGT AAA GAA GGC ACC TTC CGG AAT GAA AAC TCC CCA	558
	Gln Cys Lys Glu Gly Thr Phe Arg Asn Glu Asn Ser Pro	
	110 115 120	
40	GAG ATG TGC CGG AAG TGT AGC AGG TGC CCT AGT GGG GAA	597
	Glu Met Cys Arg Lys Cys Ser Arg Cys Pro Ser Gly Glu	
	125 130 135	

	GTC	CAA	GTC	AGT	AAT	TGT	ACG	TCC	TGG	GAT	GAT	ATC	CAG	636
	Val	Gln	Val	Ser	Asn	Cys	Thr	Ser	Trp	Asp	Asp	Ile	Gln	
						140						145		
5	TGT	GTT	GAA	GAA	TTT	GGT	GCC	AAT	GCC	ACT	GTG	GAA	ACC	675
	Cys	Val	Glu	Glu	Phe	Gly	Ala	Asn	Ala	Thr	Val	Glu	Thr	
		150					155					160		
	CCA	GCT	GCT	GAA	GAG	ACA	ATG	AAC	ACC	AGC	CCG	GGG	ACT	714
10	Pro	Ala	Ala	Glu	Glu	Thr	Met	Asn	Thr	Ser	Pro	Gly	Thr	
				165					170					
	CCT	GCC	CCA	GCT	GCT	GAA	GAG	ACA	ATG	AAC	ACC	AGC	CCA	753
	Pro	Ala	Pro	Ala	Ala	Glu	Glu	Thr	Met	Asn	Thr	Ser	Pro	
15	175					180						185		
	GGG	ACT	CCT	GCC	CCA	GCT	GCT	GAA	GAG	ACA	ATG	ACC	ACC	792
	Gly	Thr	Pro	Ala	Pro	Ala	Ala	Glu	Glu	Thr	Met	Thr	Thr	
			190					195					200	
20	AGC	CCG	GGG	ACT	CCT	GCC	CCA	GCT	GCT	GAA	GAG	ACA	ATG	831
	Ser	Pro	Gly	Thr	Pro	Ala	Pro	Ala	Ala	Glu	Glu	Thr	Met	
					205					210				
25	ACC	ACC	AGC	CCG	GGG	ACT	CCT	GCC	CCA	GCT	GCT	GAA	GAG	870
	Thr	Thr	Ser	Pro	Gly	Thr	Pro	Ala	Pro	Ala	Ala	Glu	Glu	
		215					220					225		
	ACA	ATG	ACC	ACC	AGC	CCG	GGG	ACT	CCT	GCC	TCT	TCT	CAT	909
30	Thr	Met	Thr	Thr	Ser	Pro	Gly	Thr	Pro	Ala	Ser	Ser	His	
				230					235					
	TAC	CTC	TCA	TGC	ACC	ATC	GTA	GGG	ATC	ATA	GTT	CTA	ATT	948
	Tyr	Leu	Ser	Cys	Thr	Ile	Val	Gly	Ile	Ile	Val	Leu	Ile	
35	240					245						250		

GTG CTT CTG ATT GTG TTT GTT T GAAAGACTTC ACTGTGGAAG 990  
Val Leu Leu Ile Val Phe Val  
255 259

5 AAATTCCTTC CTTACCTGAA AGGTTCAAGT AGGCGCTGGC TGAGGGCGGG 1040  
GGGCGCTGGA CACTCTCTGC CCTGCCTCCC TCTGCTGTGT TCCCACAGAC 1090  
AGAAACGCCT GCCCCTGCCC CAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1140  
10 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1180

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TGTAAAACGA CGGCCAGTTA AATAGACCTG CAATTATTAA TCT 43

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CAGGAAACAG CTATGACCAC CTGCACACCT GCAAATCCAT T 41

(2) INFORMATION FOR SEQ ID NO:7:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 49 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His  
1 5 10 15  
Leu Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly  
20 25 30  
Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys  
35 40 45  
Gly Cys Arg Lys  
49

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 48 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr Thr Asn Ala Ser Asn  
1 5 10 15

Asn Glu Pro Ser Cys Phe Pro Cys Thr Val Cys Lys Ser Asp Gln  
20 25 30

Lys His Lys Ser Ser Cys Thr Met Thr Arg Asp Thr Val Cys Gln  
5 35 40 45

Cys Lys Glu  
48

10 (2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGGAGCCGCT CATGAGGAAG TTGGGCCTCA TGGACAATGA GATAAAGGTG 50

GCTAAAGCTG AGGCAGCGGG 70

25 (2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1799 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCCACGCGTC CGCATAAATC AGCACGCGGC CGGAGAACCC CGCAATCTCT 50

GCGCCACAA AATACACCGA CGATGCCCGA TCTACTTTAA GGGCTGAAAC 100

5 CCACGGGCCT GAGAGACTAT AAGAGCGTTC CCTACCGCC ATG GAA 145  
Met Glu  
1

CAA CGG GGA CAG AAC GCC CCG GCC GCT TCG GGG GCC CGG 184  
10 Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg  
5 10 15

AAA AGG CAC GGC CCA GGA CCC AGG GAG GCG CGG GGA GCC 223  
Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala  
20 25

AGG CCT GGG CTC CGG GTC CCC AAG ACC CTT GTG CTC GTT 262  
Arg Pro Gly Leu Arg Val Pro Lys Thr Leu Val Leu Val  
30 35 40

GTC GCC GCG GTC CTG CTG TTG GTC TCA GCT GAG TCT GCT 301  
Val Ala Ala Val Leu Leu Leu Val Ser Ala Glu Ser Ala  
45 50

CTG ATC ACC CAA CAA GAC CTA GCT CCC CAG CAG AGA GCG 340  
Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln Gln Arg Ala  
55 60 65

GCC CCA CAA CAA AAG AGG TCC AGC CCC TCA GAG GGA TTG 379  
30 Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu  
70 75 80

TGT CCA CCT GGA CAC CAT ATC TCA GAA GAC GGT AGA GAT 418  
Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp  
35 85 90

	TGC	ATC	TCC	TGC	AAA	TAT	GGA	CAG	GAC	TAT	AGC	ACT	CAC	457
	Cys	Ile	Ser	Cys	Lys	Tyr	Gly	Gln	Asp	Tyr	Ser	Thr	His	
					95									100
														105
5	TGG	AAT	GAC	CTC	CTT	TTC	TGC	TTG	CGC	TGC	ACC	AGG	TGT	496
	Trp	Asn	Asp	Leu	Leu	Phe	Cys	Leu	Arg	Cys	Thr	Arg	Cys	
														110
														115
10	GAT	TCA	GGT	GAA	GTG	GAG	CTA	AGT	CCC	TGC	ACC	ACG	ACC	535
	Asp	Ser	Gly	Glu	Val	Glu	Leu	Ser	Pro	Cys	Thr	Thr	Thr	
														120
														125
														130
15	AGA	AAC	ACA	GTG	TGT	CAG	TGC	GAA	GAA	GGC	ACC	TTC	CGG	574
	Arg	Asn	Thr	Val	Cys	Gln	Cys	Glu	Glu	Gly	Thr	Phe	Arg	
														135
														140
														145
20	GAA	GAA	GAT	TCT	CCT	GAG	ATG	TGC	CGG	AAG	TGC	CGC	ACA	613
	Glu	Glu	Asp	Ser	Pro	Glu	Met	Cys	Arg	Lys	Cys	Arg	Thr	
														150
														155
25	GGG	TGT	CCC	AGA	GGG	ATG	GTC	AAG	GTC	GGT	GAT	TGT	ACA	652
	Gly	Cys	Pro	Arg	Gly	Met	Val	Lys	Val	Gly	Asp	Cys	Thr	
														160
														165
														170
30	CCC	TGG	AGT	GAC	ATC	GAA	TGT	GTC	CAC	AAA	GAA	TCA	GGC	691
	Pro	Trp	Ser	Asp	Ile	Glu	Cys	Val	His	Lys	Glu	Ser	Gly	
														175
														180
35	ATC	ATC	ATA	GGA	GTC	ACA	GTT	GCA	GCC	GTA	GTC	TTG	ATT	730
	Ile	Ile	Ile	Gly	Val	Thr	Val	Ala	Ala	Val	Val	Leu	Ile	
														185
														190
														195
40	GTG	GCT	GTG	TTT	GTT	TGC	AAG	TCT	TTA	CTG	TGG	AAG	AAA	769
	Val	Ala	Val	Phe	Val	Cys	Lys	Ser	Leu	Leu	Trp	Lys	Lys	
														200
														205
														210



	GTC	CTT	CCT	TAC	CTG	AAA	GGC	ATC	TGC	TCA	GGT	GGT	GGT	808
	Val	Leu	Pro	Tyr	Leu	Lys	Gly	Ile	Cys	Ser	Gly	Gly	Gly	
						215					220			
5	GGG	GAC	CCT	GAG	CGT	GTG	GAC	AGA	AGC	TCA	CAA	CGA	CCT	847
	Gly	Asp	Pro	Glu	Arg	Val	Asp	Arg	Ser	Ser	Gln	Arg	Pro	
		225					230					235		
	GGG	GCT	GAG	GAC	AAT	GTC	CTC	AAT	GAG	ATC	GTG	AGT	ATC	886
10	Gly	Ala	Glu	Asp	Asn	Val	Leu	Asn	Glu	Ile	Val	Ser	Ile	
				240					245					
	TTG	CAG	CCC	ACC	CAG	GTC	CCT	GAG	CAG	GAA	ATG	GAA	GTC	925
	Leu	Gln	Pro	Thr	Gln	Val	Pro	Glu	Gln	Glu	Met	Glu	Val	
	250					255					260			
	CAG	GAG	CCA	GCA	GAG	CCA	ACA	GGT	GTC	AAC	ATG	TTG	TCC	964
	Gln	Glu	Pro	Ala	Glu	Pro	Thr	Gly	Val	Asn	Met	Leu	Ser	
			265					270					275	
	CCC	GGG	GAG	TCA	GAG	CAT	CTG	CTG	GAA	CCG	GCA	GAA	GCT	1003
	Pro	Gly	Glu	Ser	Glu	His	Leu	Leu	Glu	Pro	Ala	Glu	Ala	
					280					285				
25	GAA	AGG	TCT	CAG	AGG	AGG	AGG	CTG	CTG	GTT	CCA	GCA	AAT	1042
	Glu	Arg	Ser	Gln	Arg	Arg	Arg	Leu	Leu	Val	Pro	Ala	Asn	
		290					295					300		
	GAA	GGT	GAT	CCC	ACT	GAG	ACT	CTG	AGA	CAG	TGC	TTC	GAT	1081
30	Glu	Gly	Asp	Pro	Thr	Glu	Thr	Leu	Arg	Gln	Cys	Phe	Asp	
				305					310					
	GAC	TTT	GCA	GAC	TTG	GTG	CCC	TTT	GAC	TCC	TGG	GAG	CCG	1120
	Asp	Phe	Ala	Asp	Leu	Val	Pro	Phe	Asp	Ser	Trp	Glu	Pro	
35	315					320					325			

CTC ATG AGG AAG TTG GGC CTC ATG GAC AAT GAG ATA AAG 1159  
 Leu Met Arg Lys Leu Gly Leu Met Asp Asn Glu Ile Lys  
           330                          335                          340

5 GTG GCT AAA GCT GAG GCA GCG GGC CAC AGG GAC ACC TTG 1198  
 Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu  
                           345                          350

10 TAC ACG ATG CTG ATA AAG TGG GTC AAC AAA ACC GGG CGA 1237  
 Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg  
           355                          360                          365

GAT GCC TCT GTC CAC ACC CTG CTG GAT GCC TTG GAG ACG 1276  
 Asp Ala Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr  
                           370                          375

CTG GGA GAG AGA CTT GCC AAG CAG AAG ATT GAG GAC CAC 1315  
 Leu Gly Glu Arg Leu Ala Lys Gln Lys Ile Glu Asp His  
 380                          385                          390

TTG TTG AGC TCT GGA AAG TTC ATG TAT CTA GAA GGT AAT 1354  
 Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu Gly Asn  
           395                          400                          405

GCA GAC TCT GCC WTG TCC TAAGTGTG ATTCTCTTCA GGAAGTGAGA 1400  
 Ala Asp Ser Ala Xaa Ser  
                           410 411

CCTTCCCTGG TTTACCTTTT TTCTGGAAAA AGCCCAACTG GACTCCAGTC 1450

AGTAGGAAAG TGCCACAATT GTCACATGAC CGGTACTGGA AGAAACTCTC 1500

CCATCCAACA TCACCCAGTG GATGGAACAT CCTGTAACTT TTCACTGCAC 1550

TTGGCATTAT TTTTATAAGC TGAATGTGAT AATAAGGACA CTATGGAAAT 1600

GTCTGGATCA TTCCGTTTGT GCGTACTTTG AGATTGTT TGGGATGTCA 1650  
 TTGTTTTTAC AGCACTTTTT TATCCTAATG TAAATGCTTT ATTTATTTAT 1700  
 5 TTGGGCTACA TTGTAAGATC CATCTACAAA AAAAAAAAAA AAAAAAAG 1750  
 GGCGGCCGCG ACTCTAGAGT CGACCTGCAG AAGCTTGGCC GCCATGGCC 1799

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met	Glu	Gln	Arg	Gly	Gln	Asn	Ala	Pro	Ala	Ala	Ser	Gly	Ala	Arg	1	5	10	15
Lys	Arg	His	Gly	Pro	Gly	Pro	Arg	Glu	Ala	Arg	Gly	Ala	Arg	Pro	20	25	30	
Gly	Leu	Arg	Val	Pro	Lys	Thr	Leu	Val	Leu	Val	Val	Ala	Ala	Val	35	40	45	
Leu	Leu	Leu	Val	Ser	Ala	Glu	Ser	Ala	Leu	Ile	Thr	Gln	Gln	Asp	50	55	60	
Leu	Ala	Pro	Gln	Gln	Arg	Ala	Ala	Pro	Gln	Gln	Lys	Arg	Ser	Ser	65	70	75	
Pro	Ser	Glu	Gly	Leu	Cys	Pro	Pro	Gly	His	His	Ile	Ser	Glu	Asp	80	85	90	

	Gly	Arg	Asp	Cys	Ile	Ser	Cys	Lys	Tyr	Gly	Gln	Asp	Tyr	Ser	Thr
					95					100					105
5	His	Trp	Asn	Asp	Leu	Leu	Phe	Cys	Leu	Arg	Cys	Thr	Arg	Cys	Asp
					110					115					120
	Ser	Gly	Glu	Val	Glu	Leu	Ser	Pro	Cys	Thr	Thr	Thr	Arg	Asn	Thr
					125					130					135
10	Val	Cys	Gln	Cys	Glu	Glu	Gly	Thr	Phe	Arg	Glu	Glu	Asp	Ser	Pro
					140					145					150
	Glu	Met	Cys	Arg	Lys	Cys	Arg	Thr	Gly	Cys	Pro	Arg	Gly	Met	Val
					155					160					165
15	Lys	Val	Gly	Asp	Cys	Thr	Pro	Trp	Ser	Asp	Ile	Glu	Cys	Val	His
					170					175					180
20	Lys	Glu	Ser	Gly	Ile	Ile	Ile	Gly	Val	Thr	Val	Ala	Ala	Val	Val
					185					190					195
25	Leu	Ile	Val	Ala	Val	Phe	Val	Cys	Lys	Ser	Leu	Leu	Trp	Lys	Lys
					200					205					210
	Val	Leu	Pro	Tyr	Leu	Lys	Gly	Ile	Cys	Ser	Gly	Gly	Gly	Gly	Asp
					215					220					225
	Pro	Glu	Arg	Val	Asp	Arg	Ser	Ser	Gln	Arg	Pro	Gly	Ala	Glu	Asp
					230					235					240
30	Asn	Val	Leu	Asn	Glu	Ile	Val	Ser	Ile	Leu	Gln	Pro	Thr	Gln	Val
					245					250					255
	Pro	Glu	Gln	Glu	Met	Glu	Val	Gln	Glu	Pro	Ala	Glu	Pro	Thr	Gly
35					260					265					270

Val Asn Met Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu Pro  
 275 280 285

Ala Glu Ala Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala  
 290 295 300

Asn Glu Gly Asp Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp Asp  
 305 310 315

Phe Ala Asp Leu Val Pro Phe Asp Ser Trp Glu Pro Leu Met Arg  
 320 325 330

Lys Leu Gly Leu Met Asp Asn Glu Ile Lys Val Ala Lys Ala Glu  
 335 340 345

Ala Ala Gly His Arg Asp Thr Leu Tyr Thr Met Leu Ile Lys Trp  
 350 355 360

Val Asn Lys Thr Gly Arg Asp Ala Ser Val His Thr Leu Leu Asp  
 365 370 375

Ala Leu Glu Thr Leu Gly Glu Arg Leu Ala Lys Gln Lys Ile Glu  
 380 385 390

Asp His Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu Gly Asn  
 395 400 405

Ala Asp Ser Ala Xaa Ser  
 410 411

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: Nucleic Acid

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

5

ATCAGGGACT TTCCGCTGGG GACTTTCCG 29

(2) INFORMATION FOR SEQ ID NO:13:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGGATGGGAA GTGTGTGATA TATCCTTGAT 30